



UNIVERSIDAD DE CORDOBA

FACULTAD DE CIENCIAS
GRADO DE BIOQUÍMICA
2024/25 YEAR

BIOLOGÍA MOLECULAR DE SISTEMAS

Course details

Course name: BIOLOGÍA MOLECULAR DE SISTEMAS**Code:** 101842**Degree/Master:** GRADO DE BIOQUÍMICA**Year:** 4**Field:** BIOLOGÍA MOLECULAR DE SISTEMAS**Character:** OBLIGATORIA**Duration:** FIRST TERM**ECTS Credits:** 6.0**Classroom hours:** 60**Face-to-face classroom percentage:** 40.0%**Study hours:** 90**Online platform:** <https://moodle.uco.es/>

Coordinating teacher

Name: RODRIGUEZ FRANCO, ANTONIO**Department:** BIOQUÍMICA Y BIOLOGÍA MOLECULAR**Office location:** Campus Rabanales. Edificio Severo Ochoa. Ground level**E-Mail:** bb1rofra@uco.es**Phone:** 638000485

Brief description of the contents

During the course we describe the main omics techniques such as proteomics, metabolomics, genomics, transcriptomics, metagenomics and we finish with an introduction to the methodologies and main programmes for the integration of residual data. The main proteomic techniques and the devices and the different massive sequencing methods available today are described

Prerequisites

Prerequisites established in the study plan

- to know the details of the structure and physico-chemical properties of amino acids and proteins.
- knowledge of the details of Sanger-type sequencing.
- knowledge of bioinformatics details at the level of a few genes, such as the use of different types of BLAST, the identification of coding sequences, and the handling of DNA and RNA sequences.

Recommendations

- Knowledge of technical English is recommended for the handling of scientific literature, as well as for the use of bioinformatics tools.
- recommended for the use of bioinformatics tools.
- Knowledge of the Linux operating system (Ubuntu or similar) at user level is recommended. able to download programs, install them, compile the different binaries, and manipulate files.
- It is advisable to have basic concepts of the statistical program R.
- General computer knowledge of the Windows operating system and access to browsers such as

Internet Explorer, Firefox, Chrome, Firefox, Firefox, Chrome, Firefox, Chrome, Chrome, Chrome, Chrome, Chrome, Chrome, etc.

- Knowledge of remote connections to computers.

Study programme

1. Theory contents

- Theory contents

1.-**Introduction to Molecular Systems Biology.** From traditional biology to the integrative study of biological systems. Systems Biology: definition, justification, objectives, procedures. Networks: concept and importance in Systems Biology. Importance of Systems Biology in current science.

2.-**Introduction to experimental and computational techniques.** Background of experimental techniques: from traditional biology to "omics". Experimental techniques of massive analysis ("omics"): genomics, transcriptomics, proteomics, metabolomics, metagenomics. Computational techniques (Bioinformatics). Main bioinformatics platforms in Systems Biology and their applications.

3.- **Proteomics I:** sample preparation and separation techniques. Analysis techniques. Birth and development of Proteomics. Study of the proteome. Preparation of samples for proteomics. Application of electrophoresis, chromatography, and mass spectrometry to proteomics. Main bioinformatics algorithms for the interpretation of mass spectra.

4.-**Proteomics II:** Main applications of Proteomics in Biosciences. Quantification of proteins in proteomic experiments. Proteins as biomarkers and disease diagnosis. Proteomic tools for biomarker discovery and validation. Application in the field of vaccines against infectious diseases.

5.-**Metabolomics.** Introduction to the concepts of metabolome and metabolomics. Levels of analysis of metabolites. Sample preparation for metabolomics. Applications of metabolomics to Molecular Systems Biology.

6.-**Genomics.** Genomic sequencing strategies. Description of the main massive sequencing systems (NGS). Types of sequences or reads. Sequence quality analysis and filtering. Sequencing coverage. *De novo* assembly. Concepts of contigs and scaffolds. Genomic and Transcriptomic annotations. Quality assessment of assembled genomes. Exome sequencing and targeted sequencing. Other applications.

7.-**Transcriptomics.** Approaches to the analysis of gene expression at the transcript level. Transcriptome. Types of cDNA libraries. Mappings with reference genome or transcriptome. Transcriptome assembly. Sequence mapping: mappers and pseudo-mappers. Differential expression analysis by RNA-Seq. Functional and metabolic pathway enrichments. Isoform analysis. Introduction to single-cell genomic and transcriptomic sequencing and spatial transcriptomics methods.

8.- **Metagenomics, metatranscriptomics and other techniques of relevance.** Methods for studying microbial diversity. Workflows. Definition of OTUs. Recommended programs. Applications.

9.- **Introduction to omics data integration.** Introduction to programs for the integration of different omics data: Cytoscape, paintomics, Mapman and others.

2. Practical contents

- Practical contents

Case studies and readings of selected articles. Topical reviews on Molecular Systems Biology applications that address basic and applied research issues will be selected and presented as seminars by students in the medium group classes. Forms designed to encourage discussion and establishment of concepts and ideas (whole group classes) Hands-on practice in the Bioinformatics

Classroom (medium group classes):

- Use of databases in public repositories on Proteomics resources.
- Quantitative proteomic analysis of an experiment on surface proteins in *Streptococcus pneumoniae*.
- Analysis of the quality of reads from massive sequencing systems.
- Sequence filtering of sequences from next-generation massive sequencers.
- De novo assembly of the complete genome of *E. coli* bacteria with sequences obtained from Illumina equipment. Sorting and scaffolding of the obtained contigs.
- Introduction to RNA-Seq. Mapping of reads with real mappers and pseudo-mappers. Analysis and manipulation of SAM/BAM files. Obtaining quantitative gene expression files.
- Use and applications of programs for viewing sequence alignment with reference genomes or transcriptomes (IGV, IGB or similar).
- Performance of a differential expression study by RNA-Seq using the R platform.

Bibliography

- Bibliography included in the official Moodle webpage.
- That included in the webpage <https://www.uco.es/users/bb1rofra/BiologiaSistemas/>

Methodology

General clarifications on the methodology (optional)

There will be an exam with long open questions (not multiple choice type). The use of class notes will be allowed in the exam.

If the student takes the exam and decides at that moment not to hand in the exam, he/she will be considered as failed and not as not presented.

There will be a homework in the proteomics part with which the section "Case studies" will be evaluated.

- There will be a homework in the genomics, transcriptomics and metagenomics part, whose subject will be agreed in advance with the teacher(s).

The work must be done either individually or in groups of up to 3 people maximum, and this decision must be agreed in advance with the teacher responsible for each work.

The student must have presented and evaluated the work of the course before the exam of long questions.

The marks of the practical exercises will be respected in the case that the student has to sit for a new exam due to having failed or not having sat for previous exams.

The marks of the practical exercises of previous courses will also be respected if the student has to be evaluated in subsequent courses. However, the student may redo the work if he/she considers it in his/her best interest.

To be evaluated and pass the course, the student must have made all the assignments and reached a minimum mark of 4 (out of 10) for each item.

Methodological adaptations for part-time students and students with disabilities and special educational needs

Cases will be discussed personally with the student(s) involved in order to take into account all considerations.

Face-to-face activities

Activity	Large group	Medium group	Total
<i>Information processing activities</i>	15	10	25
<i>Practical experimentation activities</i>	5	10	15
<i>Tutorial action activities</i>	5	4	9
<i>Written expression activities</i>	8	3	11
Total hours:	33	27	60

Off-site activities

Activity	Total
<i>Exercise and problem solving activities</i>	20
<i>Information processing activities</i>	30
<i>Information search activities</i>	40
Total hours	90

Results of the training and learning process

Knowledge, competencies and skills

- CB1 The ability to reason critically and self-critically.
- CB2 Know how to work on a team in a collaborative way and with shared responsibility.
- CB4 The ability to learn and work independently.
- CB6 Know how to recognize and analyse a problem, identifying its essential components, and plan a scientific strategy to solve it.
- CB7 Know how to use the basic computer tools for communication, information searches, and data processing in one's professional activity.
- CE24 Possess the mathematical, statistical, and computer skills to obtain, analyse, and interpret data, and to understand simple models of biological systems and processes at the cellular and molecular levels.
- CE25 Know how to search for, obtain and interpret information from the main biological databases (genomic, transcriptomic, proteomic, metabolomic and similar ones derived from other massive analyses) and bibliographic data, and use basic bioinformatics tools.
- CE26 Have the ability to pose and solve questions and problems in the field of

Biochemistry and Molecular Biology through scientific hypotheses that can be empirically examined.

- CE27 Understand the basic aspects of the design of experiments in the areas of Biochemistry and Molecular Biology, understanding the limitations of experimental approaches.
- CE29 Acquire basic training in the development of projects, including the ability to carry out a study in the areas of Biochemistry and Molecular Biology, to critically interpret the results obtained, and to evaluate the conclusions reached.

Assessment methods and instruments

Intended learning outcomes	Examination	Means of practical execution	Students assignments
CB1		X	
CB2		X	
CB4		X	
CB6		X	
CB7	X		
CE24	X		
CE25			X
CE26			X
CE27			X
CE29			X
Total (100%)	60%	20%	20%
Minimum grade (*)	4	4	4

(*)Minimum mark (out of 10) needed for the assessment tool to be weighted in the course final mark. In any case, final mark must be 5,0 or higher to pass the course.

General clarifications on instruments for evaluation:

There will be an exam with long open questions (not multiple choice type). The use of class notes will be allowed in the exam.

If the student takes the exam and decides at that moment not to hand in the exam, he/she will be considered as failed and not as not presented.

There will be a homework in the proteomics part with which the section "students assignments" will be evaluated.

- There will be a homework in the genomics, transcriptomics and metagenomics part, whose subject will be agreed in advance with the teacher(s).

The work must be done either individually or in groups of up to 3 people maximum, and this decision must be agreed in advance with the teacher responsible for each work.

The student must have presented and evaluated the work of the course before the exam of long questions.

The marks of the practical exercises will be respected in the case that the student has to sit for a new exam due to having failed or not having sat for previous exams.

The marks of the practical exercises of previous courses will also be respected if the student has to be evaluated in subsequent courses. However, the student may redo the work if he/she considers it in his/her best interest.

To be evaluated and pass the course, the student must have made all the assignments and reached a minimum mark of 4 (out of 10) for each item.

Clarifications on the methodology for part-time students and students with disabilities and special educational needs:

Cases will be discussed personally with the student(s) involved in order to take into account all considerations.

Clarifications on the evaluation of the extraordinary call and extra-ordinary call for completion studies:

In the evaluation of the extraordinary call and in the extraordinary call for completion of studies, the grades of all the instruments of previous and present courses that have been taken will be kept. In addition, it will be evaluated in the same way as in the ordinary exams.

Qualifying criteria for obtaining honors:

A score of 9.5 must be met or exceeded in order to obtain an honors degree

Sustainable development goals

Good health and well-being

Other Faculty

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The methodological strategies and the evaluation system contemplated in this Teaching Guide will respond to the principles of equality and non-discrimination and must be adapted according to the needs presented by students with disabilities and special educational needs in the cases that are required. Students must be informed of the risks and measures that affect them, especially those that may have serious or very serious consequences (article 6 of the Safety, Health and Welfare Policy; BOUCO 23-02-23).
